2/52 Fig.1(i)	3/52 Fig.1(ii)
4/52 Fig.1(iii)	5/52 Fig.1(iv)

```
1       TCGGCCTCC GAAACC ATG AAC TTT CTG
                         Met Asn Phe Leu
                           1

50      CTT GCC TTG CTG CTC TAC CTC CAC
        Leu Ala Leu Leu Leu Tyr Leu His
                    15

98      CCC ATG GCA GAA GGA GGA GGG CAG
        Pro Met Ala Glu Gly Gly Gly Gln
                30                  35

146     ATG GAT GTC TAT CAG CGC AGC TAC
        Met Asp Val Tyr Gln Arg Ser Tyr
             45                 50

194     GAC ATC TTC CAG GAG TAC CCT GAT
        Asp Ile Phe Gln Glu Tyr Pro Asp
         60                 65

242     TCC TGT GTG CCC CTG ATG CGA TGC
        Ser Cys Val Pro Leu Met Arg Cys
                        80

290     CTC GAG TGT GTG CCC ACT GAG GAG
        Leu Glu Cys Val Pro Thr Glu Glu
                    95

338     CGG ATC AAA CCT CAC CAA GGC CAG
        Arg Ily Lys Pro His Gln Gly Gln
                110                 115
```

Fig.1(i)

```
CTG TCT TGG GTG CAT TGG AGC                                    49
Leu Ser Trp Val His Trp Ser
  5                  10

CAT GCC AAG TGG TCC CAG GCT GCA                                97
His Ala Lys Trp Ser Gln Ala Ala
 20                  25

AAT CAT CAC GAA GTG GTG AAG TTC                               145
Asn His His Glu Val Val Lys Phe
                40

TGC CAT CCA ATC GAG ACC CTG GTG                               193
Cys His Pro Ile Glu Thr Leu Val
            55

GAG ATC GAG TAC ATC TTC AAG CCA                               241
Glu Ile Glu Tyr Ile Phe Lys Pro
        70                  75

GGG GGC TGC TGC AAT GAC GAG GGC                               289
Gly Gly Cys Cys Asn Asp Glu Gly
    85                  90

TCC AAC ATC ACC ATG CAG ATT ATG                               337
Ser Asn Ile Thr Met Gln Ile Met
100                 105

CAC ATA GGA GAG ATG AGC TTC CTA                               385
His Ile Gly Glu Met Ser Phe Leu
            120
```

Fig.1(ii)

```
386   CAG CAC AAC AAA TGT GAA TGC AGA
      Gln His Asn Lys Cys Glu Cys Arg
          125                 130

434   GAA AAT CCC TGT GGG CCT TGC TCA
      Glu Asn Pro Cys Gly Pro Cys Ser
      140                 145

482   CAA GAT CCG CAG ACG TGT AAA TGT
      Gln Asp Pro Gln Thr Cys Lys Cys
                      160

530   TGC AAG GCG AGG CAG CTT GAG TTA
      Cys Lys Ala Arg Gln Leu Glu Leu
                  175

578   AAG CCG AGG CGG TGAGCCGGGC AGGAG
      Lys Pro Arg Arg
              190

630   GAACCAGATC TCTCACCAGG
```

Fig.1(iii)

```
CCA AAG AAA GAT AGA GCA AGA CAA                                  433
Pro Lys Lys Asp Arg Ala Arg Gln
            135

GAG CGG AGA AAG CAT TTG TTT GTA                                  481
Glu Arg Arg Lys His Leu Phe Val
        150                 155

TCC TGC AAA AAC ACA GAC TCG CGT                                  529
Ser Cys Lys Asn Thr Asp Ser Arg
    165                 170

AAC GAA CGT ACT TGC AGA TGT GAC                                  577
Asn Glu Arg Thr Cys Arg Cys Asp
180                 185

GAAGG AGCCTCCCTC AGCGTTTCGG                                      629
```

649

Fig.1(iv)

7/52 Fig.2(i)	8/52 Fig.2(ii)
9/52 Fig 2(iii)	10/52 Fig 2(iv)
11/52 Fig 2(v)	12/52 Fig 2(vi)

```
1       CC ATG AGC CCT CTG CTC CGC CGC
            Met Ser Pro Leu Leu Arg Arg
              1               5

48      CTG GCC CCC GCC CAG GCC CCT GTC
        Leu Ala Pro Ala Gln Ala Pro Val
                        20

96      CAG AGG AAA GTG GTG TCA TGG ATA
        Gln Arg Lys Val Val Ser Trp Ile
                    35

144     CAG CCC CGG GAG GTG GTG GTG CCC
        Gln Pro Arg Glu Val Val Val Pro
                50                  55

192     GTG GCC AAA CAG CTG GTG CCC AGC
        Val Ala Lys Gln Leu Val Pro Ser
            65                  70

240     GGC TGC TGC CCT GAC GAT GGC CTG
        Gly Cys Cys Pro Asp Asp Gly Leu
         80                 85

288     CAA GTC CGG ATG CAG ATC CTC ATG
        Gln Val Arg Met Gln Ile Leu Met
                        100

336     GGG GAG ATG TCC CTG GAA GAA CAC
        Gly Glu Met Ser Leu Glu Glu His
                    115
```

Fig.2(i)

```
CTG CTG CTC GCC GCA CTC CTG CAG                    47
Leu Leu Leu Ala Ala Leu Leu Gln
          10                  15

TCC CAG CCT GAT GCC CCT GGC CAC                    95
Ser Gln Pro Asp Ala Pro Gly His
     25                  30

GAT GTG TAT ACT CGC GCT ACC TGC                   143
Asp Val Tyr Thr Arg Ala Thr Cys
 40                  45

TTG ACT GTG GAG CTC ATG GGC ACC                   191
Leu Thr Val Glu Leu Met Gly Thr
                60

TGC GTG ACT GTG CAG CGC TGT GGT                   239
Cys Val Thr Val Gln Arg Cys Gly
            75

GAG TGT GTG CCC ACT GGG CAG CAC                   287
Glu Cys Val Pro Thr Gly Gln His
          90                  95

ATC CGG TAC CCG AGC AGT CAG CTG                   335
Ile Arg Tyr Pro Ser Ser Gln Leu
    105                 110

AGC CAG TGT GAA TGC AGA CCT AAA                   383
Ser Gln Cys Glu Cys Arg Pro Lys
120                 125
```

Fig. 2(ii)

384	AAA Lys	AAG Lys	GAC Asp 130	AGT Ser	GCT Ala	GTG Val	AAG Lys	CCA Pro 135
432	CGT Arg	CCC Pro 145	CAG Gln	CCC Pro	CGT Arg	TCT Ser	GTT Val 150	CCG Pro
480	CCC Pro 160	TCC Ser	CCA Pro	GCT Ala	GAC Asp	ATC Ile 165	ACC Thr	CAT His
528	GCC Ala	CAC His	GCT Ala	GCA Ala	CCC Pro 180	AGC Ser	ACC Thr	ACC Thr
576	GCT Ala	GCC Ala	GCT Ala	GCC Ala 195	GAC Asp	GCC Ala	GCA Ala	GCT Ala

Fig. 2(iii)

```
GAC AGG GCT GCC ACT CCC CAC CAC                    431
Asp Arg Ala Ala Thr Pro His His
                140

GGC TGG GAC TCT GCC CCC GGA GCA                    479
Gly Trp Asp Ser Ala Pro Gly Ala
            155

CCC ACT CCA GCC CCA GGC CCC TCT                    527
Pro Thr Pro Ala Pro Gly Pro Ser
        170                 175

AGC GCC CTG ACC CCC GGA CCT GCC                    575
Ser Ala Leu Thr Pro Gly Pro Ala
    185                 190

TCC TCC GTT GCC AAG GGC GGG GCT T                  624
Ser Ser Val Ala Lys Gly Gly Ala
200                 205
```

Fig. 2(iv)

```
 625   AGAGCTCAAC CCAGACACCT GCAGGTGCCG
 685   GACTCAGCAG GGTGACTTGC CTCAGAGGCT
 745   GGTAAAAAAC AGCCAAGCCC CCAAGACCTC
 805   GCCTCTCAGA GGGCTCTTCT GCCATCCCTT
 865   GAGTTGGAAG AGGAGACTGG GAGGCAGCAA
 825   GGAGTACTGT CTCAGTTTCT AACCACTCTG
 985   CTCCCCTCAC TAAGAAGACC CAAACCTCTG
1045   CTGTGACCCC CAACCCTGAT AAAAGAGATG
```

Fig. 2(v)

GAAGCTGCGA AGGTGACACA TGGCTTTTCA	684
ATATCCCAGT GGGGGAACAA AGGGGAGCCT	744
AGCCCAGGCA GAAGCTGCTC TAGGACCTGG	804
GTCTCCCTGA GGCCATCATC AAACAGGACA	864
GAGGGGTCAC ATACCAGCTC AGGGGAGAAT	924
TGCAAGTAAG CATCTTACAA CTGGCTCTTC	984
CATAATGGGA TTTGGGCTTT GGTACAAGAA	1044
GAAGGAAAAA AAAAAAAAAA	1094

Fig.2(vi)

13/52

14/52 Fig. 3(i)	15/52 Fig. 3(ii)

14/52

```
>VEGF_HUMAN VEGF_HUMAN  VASCULAR ENDOTHELIAL
            (VASCULAR 215 AA.
            LENGTH = 215

 SCORE = 181 (92.4 BITS), EXPECT = 6.4e-20,
 IDENTITIES = 33/75 (44%), POSITIVES = 48/75

QUERY:    31 HQRKVVSWIDVYTRATCQPREVVVPLTVEL
             +++ VV  +DVY R+ C+P E +V +  E
SBJCT:    36 NHHEVVKFMDVYQRSYCHPIETLVDIFQEY

QUERY:    91 PTGQHQVRMQILMIR 105
             PT +  + MQI+ I+
SBJCT:    96 PTEESNITMQIMRIK 110

 SCORE = 76  (38.8 BITS), EXPECT = 0.0011,
 IDENTITIES = 12/19 (63%), POSITIVES = 16/19

QUERY:   110 QLGEMSLEEHSQCECRPKK 128
             ++GEMS  +H+ CECRPKK
SBJCT:   116 HIGEMSFLQHNKCECRPKK 134

 SCORE = 72  (36.8 BITS), EXPECT = 0.0046,
 IDENTITIES = 14/21 (66%), POSITIVES = 15/21

QUERY:   202 RCQGRGLELNPDTCRCRKLRR 222
             RC +R LELN  TCRC K RR
SBJCT:   195 RCKARQLELNERTCRCDKPRR 215

 SCORE = 46  (23.5 BITS), EXPECT = 47.,
 IDENTITIES =  6/10 (60%), POSITIVES = 9/10

QUERY:   187 DPRTCRCRCR 196
             DP+TC+C C+
SBJCT:   181 DPQTCKCSCK 190
```

Fig.3(i)

GROWTH FACTOR PRECURSOR (VEGF)

P = 6.4e-20
(64%)

MGTVAKQLVPSCVTVQRCGGCCPDDGLECV 90
+ PSCV + RCGGCC D+GLECV
PDEIEYIFKPSCVPLMRCGGCCNDEGLECV 95

POISSON P(2) = 9.1e-12
(84%)

POISSON P(3) = 3.6e-18
(71%)

POISSON P(4) = 7.3e-10
(90%)

Fig. 3(i)

17/52 Fig.4(i)	18/52 Fig.4(ii)
19/52 Fig.4(iii)	20/52 Fig.4(iv)

Gap Weight:3.00 Average Match:1.000
Length Weight:0.100 Average Mismatch:-0.900
Quality:100.9 Length:739
Ratio:0.175 Gaps:30
Percent Similarity:69.703 Percent Identity:69.703

```
 28    ATGAGCCCTCTGCTCCGCCGCCTGC
       ||||  |  ||||||      | ||
 17    ATGAACTTTCTGCT.....GTCT..

 68    TGCAGCTGGCCCCCGCCCAGGCCCC
       |||  |||   ||  |  |||  |||
 57    TGCTGCTCTACCTCCACCATGCCAA

118    CACCAGAGGA..............
            |||||
106    AGAAGGAGGAGGGCAGAATCATCAC

140    GTGTATACTCGC.GCTACCTGCCAG
       ||  |||   |||  ||||  ||||||
152    GTCTATCAGCGCAGCTA.CTGCCAT

194    T....GA.....CTGTGGAGCTCAT
       |     ||      |||  |||  ||
201    TCCAGGAGTACCCTGATGAGATCGA

235    CCCAGCTGCGTGACTGTGCAGCGCT
       ||   |||  |||  |  ||  |||  |
239    CCATCCTGTGTGCCCCTGATGCGAT

285    CCTGGAGTGTGTGCCCACTGGGCAG
       |||||||||||||||||||  |  ||
289    CCTGGAGTGTGTGCCCACTGAGGAG
```

Fig.4(i)

```
TGCTCGCCGCACT..........CC      67
   | |   ||| |             |
...TGGGTGCATTGGAGCCTTGCCT      56

TGTCTCCCAGCCTGATGCCCCTGGC      117
    |||||| |||   ||| ||||
GTGGTCCCAGGCTGCA.CCCATGGC      105

.AAGTGGTG....TCATGGATAGAT      147
 ||||||||    |||||    |||
GAAGTGGTGAAGTTCATG....GAT      151

CCCCGGGAG...GTGGTGGTGCCCT      193
||     |||     ||||||     ||
CCAATCGAGACCCTGGTGGACATCT      200

GGGCACCGTGGCCAAACAGCTGGTG      234
|   ||  |  |    |||           |
GTACATCTT...CAA.........G      238

GTGGTGGCTGCTGCCCTGACGATGG      284
|  ||  ||||||||||  ||||||  ||
GCGGGGGCTGCTGCAATGACGAGGG      288

CACCAAGTCCGGATGCAGAT.....      329
   |  |   ||    ||||||||
TCCAACATCACCATGCAGATTATGC      338
```

Fig.4(ii)

```
330    .........CCTCATGATCCGGTACC
                |||||              |
339    GGATCAAACCTCA............C

369    GTCCCTGGAAGAACACAGCCAGTGT
       |   | |    | | |||| | | |||
376    GAGCTTCCTACAGCACAACAAATGT

419    GTGCTGTGAAGCCAGACAGGGCTGC
       |          |||  |||||  |
423    G........AGCAAGACAAG.....

469    CGTTCTGTTCCGGGCTGGGACTCTG
           | ||   ||   |||   ||
443    ...TGTGGGCCTTGCTCAGA.....

519    CATCACCCATCCCACTCCAGCCCCA

468    .........................

569    GC..........ACCACCAGCGCCC
       ||             ||  |
469    GCATTTGTTTGTACAA.........

609    TGCCGACGCCGCAGCTTCCTCCGTT
       ||  |  |    | |||  ||    ||||
509    TG.CAAAAACACAGACTC..GCGTT

657    AACCCAGACACCTGCAGGTGCCGGA
       |||   |
554    AACGAACGTACTTGCAGATGTGACA
```

Fig.4(iii)

```
CGAGCAGTCAGC...TGGGGGAGAT      368
|  ||   |  ||||    |  ||  |||||
CAAG..GCCAGCACATAGGAGAGAT      375

GAATGCAGACCTAAAAAAAAGGACA      418
||||||||||||   |||  ||  ||  |
GAATGCAGACC...AAAGAAAGATA      422

CACTCCCCACCACCGTCCCCAGCCC      468
             |   ||||
...........AAAATCCC......      442

CCCCCGGAGCACCCTCCCCAGCTGA      518
    |||||  |
...GCGGAGAA.............      467

GGCCCCTCTGCCCACGCTGCACCCA      568
                          |
.........................A     468

TGACCCCCGGACCTGCCGCTGCCGC      608
 ||  ||  |  |||  ||     ||    |
.GATCCGCAGACGTGTAAATGTTCC      508

GCCAAGGGCGGGGC..TTAGAGCTC      656
||     ||||  |||    |  |||  |
GC..AAGGCGAGGCAGCTTGAGTTA      553

AGCTGCGAAGGTGA                 695

AGCCGAGGCGGTGA                 592
```

Fig.4(iv)

21/52

22/52 Fig.5(i)	23/52 Fig.5(ii)	24/52 Fig.5(iii)
25/52 Fig.5(iv)	26/52 Fig.5(v)	27/52 Fig.5(vi)

```
165SOMSQ.MSF.msf MSF:687
Type: D Tuesday, June 20, 1995
Check:3140

                      1
      VEGF165   ATGAACTTTCTGCTGTCTTGGGTG
       SOM175   ATGAGCCCTCTGCTCCGCCGCCTG
     SOM175-e6  ATGAGCCCTCTGCTCCGCCGCCTG
   SOM175-e6&7  ATGAGCCCTCTGCTCCGCCGCCTG
     SOM175-e4  ATGAGCCCTCTGCTCCGCCGCCTG

                     81
      VEGF165   CACCCATGGCAGAAGGAGGAGGGC
       SOM175   TGCCCCTGGCCACCAGAGGAAAGT
     SOM175-e6  TGCCCCTGGCCACCAGAGGAAAGT
   SOM175-e6&7  TGCCCCTGGCCACCAGAGGAAAGT
     SOM175-e4  TGCCCCTGGCCACCAGAGGAAAGT

                    161
      VEGF165   CCAATCGAGACCCTGGTGGACATC
       SOM175   GTGGTGGTGCCCTTGACTG.TGGA
     SOM175-e6  GTGGTGGTGCCCTTGACTG.TGGA
   SOM175-e6&7  GTGGTGGTGCCCTTGACTG.TGGA
     SOM175-e4  GTGGTGGTGCCCTTGACTG.TGGA

                    241
      VEGF165   GATGCGATGCGGGGGCTGCTGCAA
       SOM175   GCAGCGCTGTGGTGGCTGCTGCCC
     SOM175-e6  GCAGCGCTGTGGTGGCTGCTGCCC
   SOM175-e6&7  GCAGCGCTGTGGTGGCTGCTGCCC
     SOM175-e4  GCAGCGCTGTGGTGGCTGCTGCCC
```

Fig.5(i)

```
CATTGGAGCCTTGCCTTGCTGCTCTACC
CTGCTCGCCGCACTCCTGCAGCTGGCCC
CTGCTCGCCGCACTCCTGCAGCTGGCCC
CTGCTCGCCGCACTCCTGCAGCTGGCCC
CTGCTCGCCGCACTCCTGCAGCTGGCCC

AGAATCATCACGAAGTGGTGAAGTTCAT
GGTGTCATGGATAGATGTGTATACTCGC
GGTGTCATGGATAGATGTGTATACTCGC
GGTGTCATGGATAGATGTGTATACTCGC
GGTGTCATGGATAGATGTGTATACTCGC

TTCCAGGAGTACCCTGATGAGATCGAGT
GCTCATGGGCACCGTGGCCAAAC..AGC
GCTCATGGGCACCGTGGCCAAAC..AGC
GCTCATGGGCACCGTGGCCAAAC..AGC
GCTCATGGGCACCGTGGCCAAAC..AGC

TGACGAGGGCCTGGAGTGTGTGCCCACT
TGACGATGGCCTGGAGTGTGTGCCCACT
TGACGATGGCCTGGAGTGTGTGCCCACT
TGACGATGGCCTGGAGTGTGTGCCCACT
TGACGATGGCCTGGAGTGTGTGCCCACT
```

Fig. 5(ii)

```
                                                          80
TCCACCATGCCAAGTGGTCCCAGGCTG.
CCGCCCAGGCCCCTGTCTCCCAGCCTGA
CCGCCCAGGCCCCTGTCTCCCAGCCTGA
CCGCCCAGGCCCCTGTCTCCCAGCCTGA
CCGCCCAGGCCCCTGTCTCCCAGCCTGA

                                                         160
GGATGTCTATCAGCGCAGCTACTGCCAT
G.....CTACCTGC.CAGCC.CCGGGAG
G.....CTACCTGC.CAGCC.CCGGGAG
G.....CTACCTGC.CAGCC.CCGGGAG
G.....CTACCTGC.CAGCC.CCGGGAG

                                                         240
ACATCTTCAAGCCATCCTGTGTGCCCCT
TGGTGCCCAG......CTGCGTGACTGT
TGGTGCCCAG......CTGCGTGACTGT
TGGTGCCCAG......CTGCGTGACTGT
TGGTGCCCAG......CTGCGTGACTGT

                                                         320
GAGGAGTCCAACATCACCATGCAGATTA
GGGCAGCACCAAGTCCGGATGCAGATCC
GGGCAGCACCAAGTCCGGATGCAGATCC
GGGCAGCACCAAGTCCGGATGCAGATCC
GGGCAGCACCAAGTCCGGATGCAGA...
```

Fig.5(iii)

```
                    321
VEGF165     TGCGGATCAAACCTCACCAAGGCC
SOM175      TCATGATCCGG...TACCCGAGCA
SOM175-e6   TCATGATCCGG...TACCCGAGCA
SOM175-e6&7 TCATGATCCGG...TACCCGAGCA
SOM175-e4   ........................

                    401
VEGF165     AAGAAAGATAG........AGCAA
SOM175      AAAAAGGACAGTGCTGTGAAGCCA
SOM175-e6   AAAAAGGACAGTGCTGTGAAGCCA
SOM175-e6&7 AAAAAGGACAGTGCTGTGAAGCCA
SOM175-e4   AAAAAGGACAGTGCTGTGAAGCCA

                    481
VEGF165     ..........AAGCA........
SOM175      CTCTGCCCCCGGAGCACCCTCCCC
SOM175-e6   ........................
SOM175-e6&7 ........................
SOM175-e4   CTCTGCCCCCGGAGCACCCTCCCC

                    561
VEGF165     A..............GATCCGCA
SOM175      GCACCACCAGCGCCCTGACCCCCG
SOM175-E6   GCACCACCAGCGCCCTGACCCCCG
SOM175-e6&7 ........................
SOM175-e4   GCACCACCAGCGCCCTGACCCCCG

                    641
VEGF165     TTGAGTTAAACGAACGTACTTGCA
SOM175      TAGAGCTCAACCCAGACACCTGCA
SOM175-e6   TAGAGCTCAACCCAGACACCTGCA
SOM175-e6&7 ........................
SOM175-e4   TAGAGCTCAACCCAGACACCTGCA
```

Fig.5(iv)

```
AGCACATAGGAGAGATGAGCTTCCTACA
GTCAGCTGGGGGAGATGTCCCTGGAAGA
GTCAGCTGGGGGAGATGTCCCTGGAAGA
GTCAGCTGGGGGAGATGTCCCTGGAAGA
.............................

GACAAGAA....AATCCCTGTGG.....
GACAGGGCTGCCACTCCCCACCACCGTC
GATAG.......................
GATAG.......................
GACAGGGCTGCCACTCCCCACCACCGTC

.............................
AGCTGACATCACCCATCCCACTCCAGCC
.........................CC
.............................
AGCTGACATCACCCATCCCACTCCAGCC

GACGTGTAAATGTTCCTGCAAAAAC.AC
GACCTGCCGCTGCCGCTGCCGACGCCGC
GACCTGCCGCTGCCGCTGCCGACGCCGC
.............................
GACCTGCCGCTGCCGCTGCCGACGCCGC

                          687
GATGTGACAAGCCGAGGCGGTGA
GGTGCCGGAAGCTGCGAAGGTGA
GGTGCCGGAAGCTGCGAAGGTGA
.GTGCCGGAAGCTGCGAAGGTGA
GGTGCCGGAAGCTGCGAAGGTGA
```

Fig.5(v)

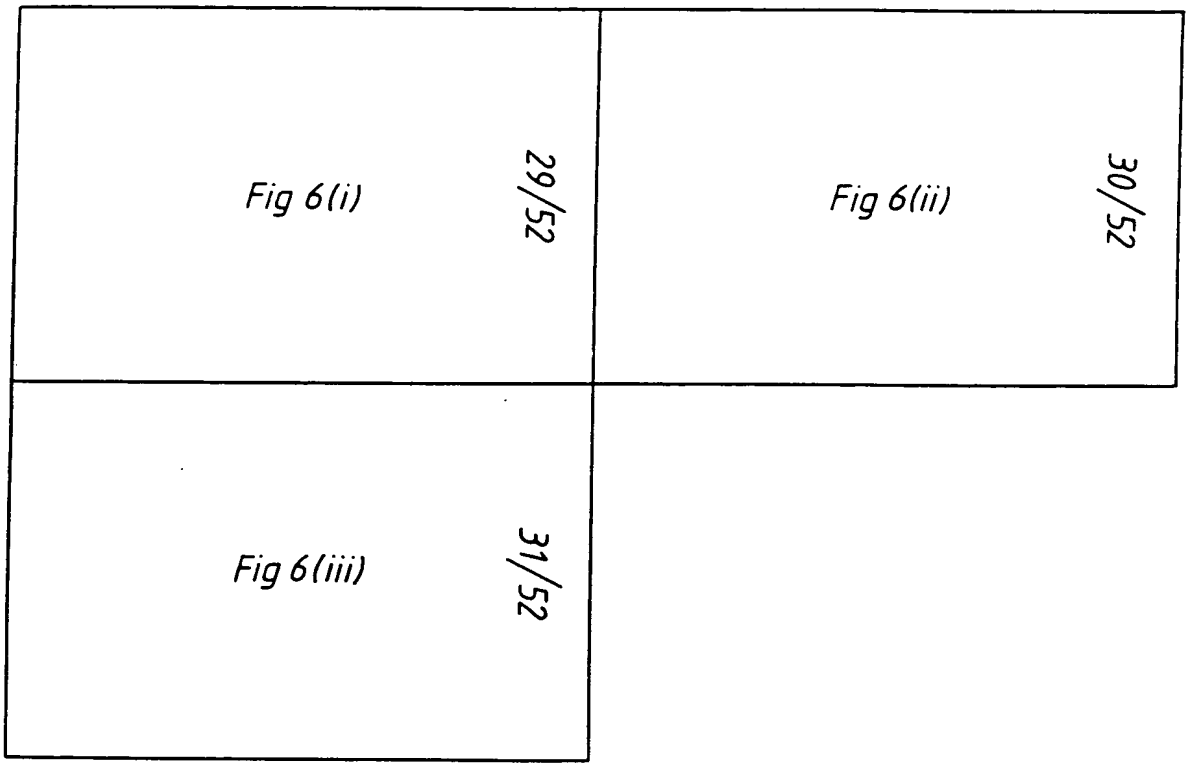
```
                                                    400
GCACAACAAATGTGAATGCAGACC...A
ACACAGCCAGTGTGAATGCAGACCTAAA
ACACAGCCAGTGTGAATGCAGACCTAAA
ACACAGCCAGTGTGAATGCAGACCTAAA
.......................CCTAAA

                                                    480
.........GCCTTGCTCAGAGCGGAGA
CCCAGCCCCGTTCTGTTCCGGGCTGGGA
.............................
.............................
CCCAGCCCCGTTCTGTTCCGGGCTGGGA

                                                    560
.........TTTGTT.....TGTAC..A
CCAGGCCCCTCTGCCCACGCTGCACCCA
CCAGGCCCCTCTGCCCACGCTGCACCCA
.............................
CCAGGCCCCTCTGCCCACGCTGCACCCA

                                                    640
AGACTCG..CGTTGCAAGGCGAGGCAGC
AGCTTCCTCCGTTGCCAAGGGCGGGGCT
AGCTTCCTCCGTTGCCAAGGGCGGGGCT
.............................
AGCTTCCTCCGTTGCCAAGGGCGGGGCT
```

Fig.5(vi)



WO 96/27007
PCT/US96/00094


```
VEGF165        M N F L L S W V H W S L A L L L Y L H H A K W S Q A A P
SOM175Short    M S P L L R R L L . . L A A L L Q L A P A Q . . . . A P

VEGF165        I F Q E Y P D E I E Y I F K P S C V P L M R C G G C C N
SOM175Short    L T V E L M G T V A K Q L V P S C V T V Q R C G G C C P

VEGF165        F L Q H N K C E C R P K K . . . . . D R A . . . . . .
SOM175Short    L E E H S Q C E C R P K K K D S A V K P D R A A T P H H

VEGF165        C K C S C K N T D S R C K A R Q L E L N E R T C R C D K
SOM175Short    H A A P S T T S A L T P G P A A A A A A D A A A S S V A K

OR...

VEGF165        M N F L L S W V H W S L A L L L Y L H H A K W S Q A A P
SOM175Long     M S P L L R R L L . . L A A L L Q L A P A Q . . . . A P

VEGF165        I F Q E Y P D E I E Y I F K P S C V P L M R C G G C C N
SOM175Long     L T V E L M G T V A K Q L V P S C V T V Q R C G G C C P

VEGF165        F L Q H N K C E C R P K K . . . . . D R A . . . . . .
SOM175Long     L E E H S Q C E C R P K K K D S A V K P D R A A T P H H

VEGF165        G P C S E R R K H L F V Q D P Q T C K C S C K N T D S .
SOM175Long     P R C T Q H H Q R . . . P D P R T C R C R C R R R S F L
```

Fig.6(i)

0847655 88

PCT/AU96/00094
08/765588

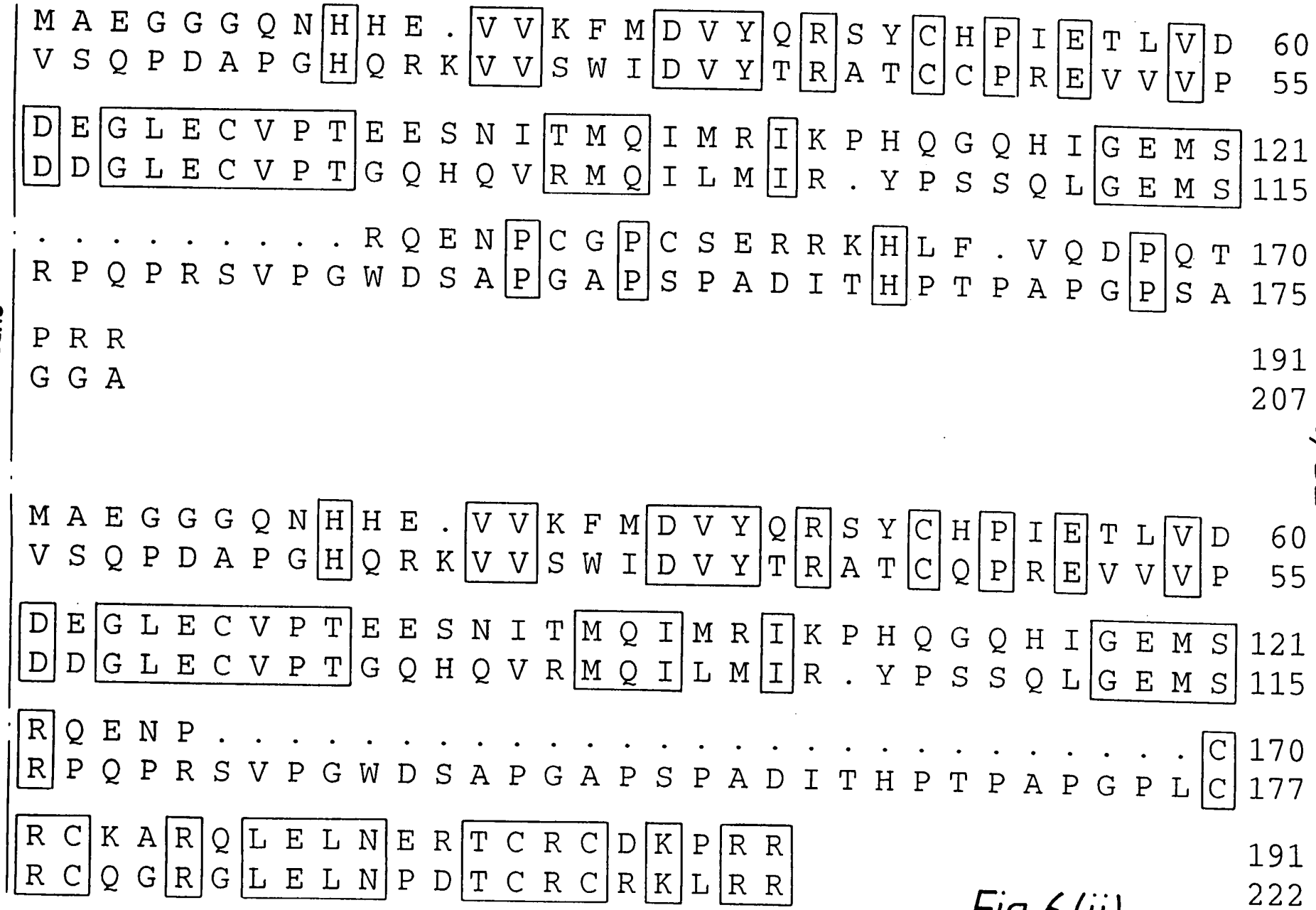


Fig. 6(ii)

Areas of 100% homology are boxed and conserved residues thought to be involved in homodimerisation are underlined.
The VEGF sequence depicted includes the 26 amino acid leader sequence (removal of which gives rise to mature $VEGF_{165}$) giving a total length of 191 amino acids.

Homology of SOM175 to $VEGF_{165}$ is 27% (33%) at the protein level, however within this are blocks of 100% homology. In particular, many structural residues are conserved including those thought to be involved in homodimerisation of VEGF (by comparison with PDGF).

ie. Cysteine-47
Proline-70, Cysteine-72, Valine-74
Arginine-77, Cystein-78, Glycine-80, Cysteines-81 & 82
Cysteine-89, Proline-91
Cysteines 122 & 124

Fig.6(iii)

08/765588
PCT/AU96/00094

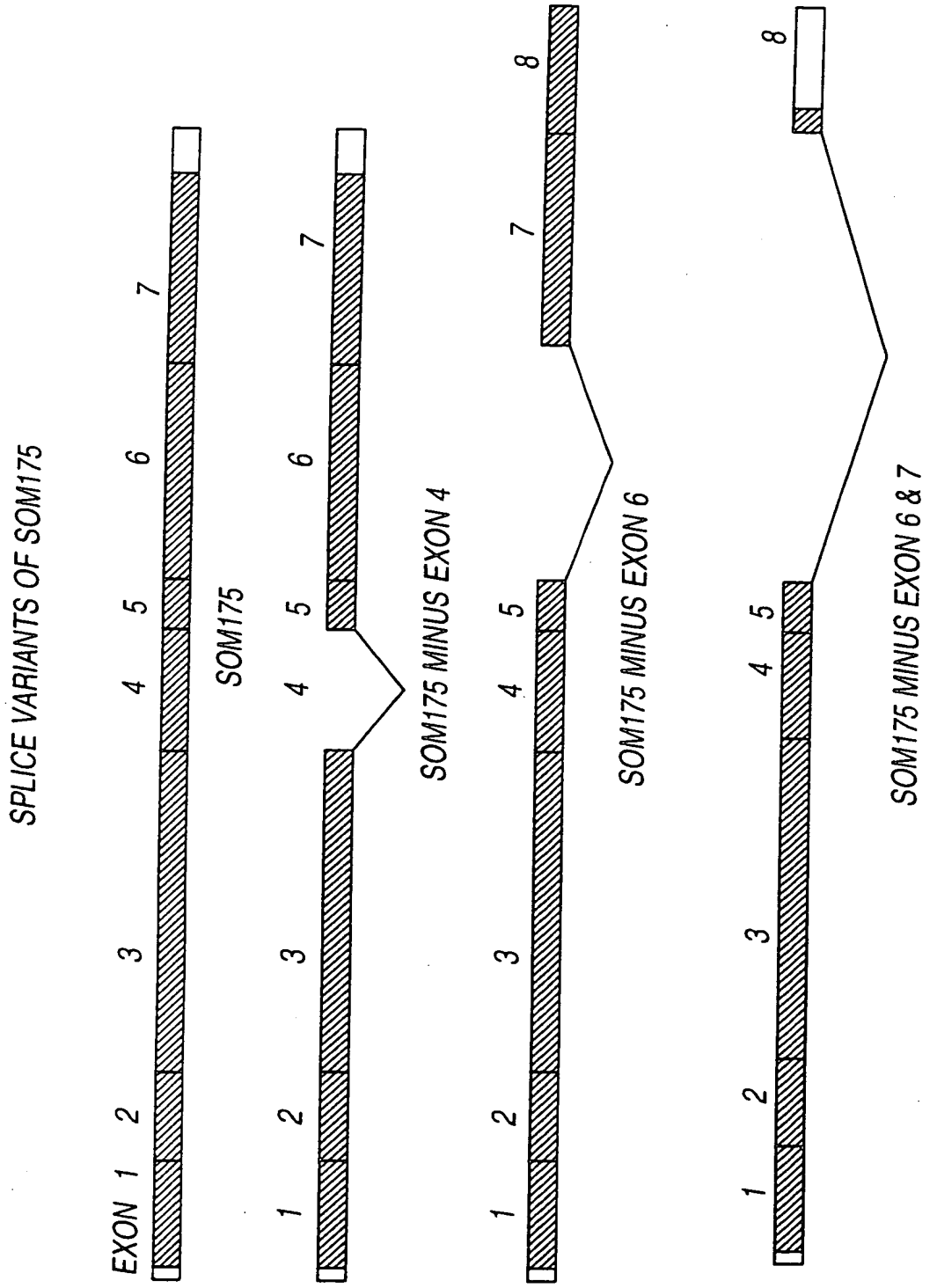


Fig. 7

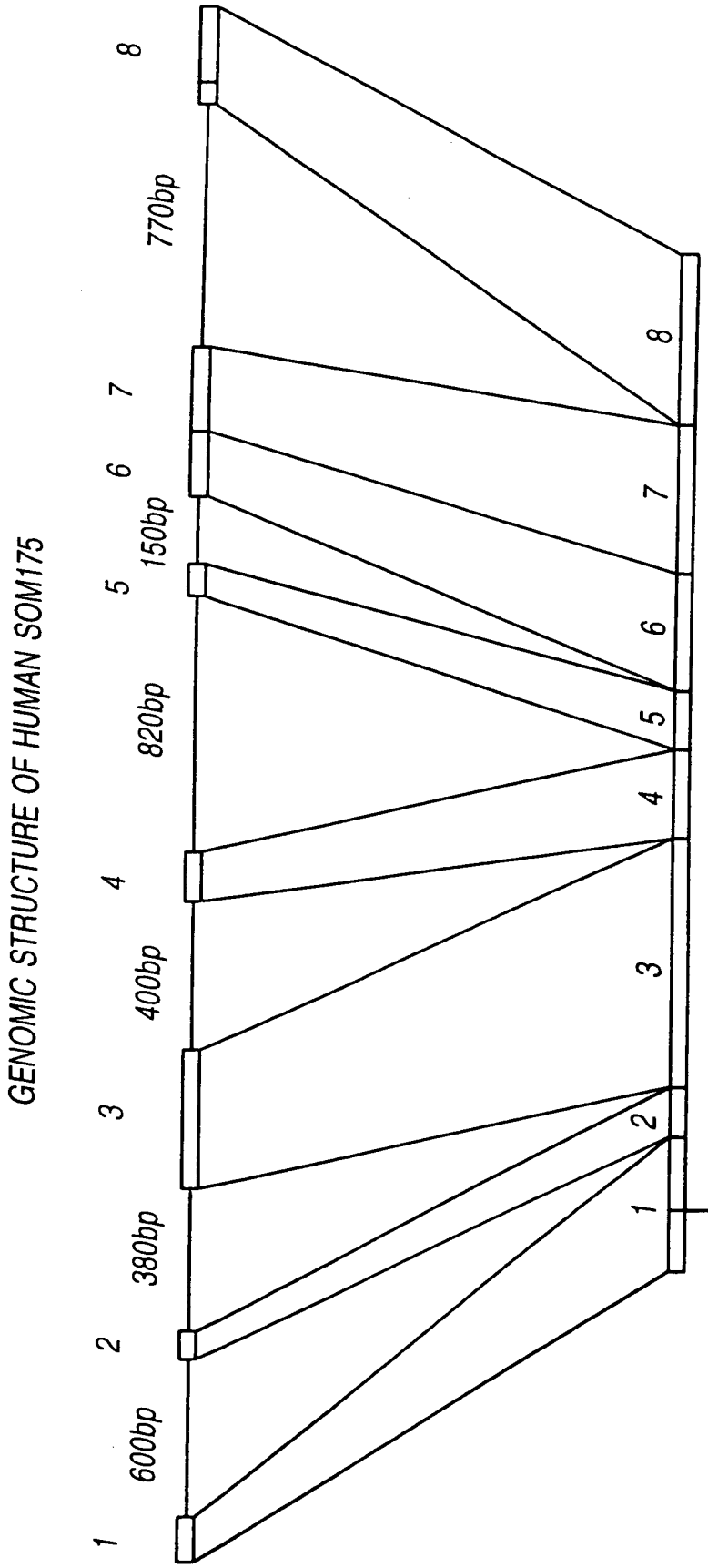


Fig.8A

5'UTR...	**ATG**AGG	*Exon 1	(60bp)	GGCCAG	gtacgtgagg
tctcccacag	GCCCCT	Exon 2	(43bp)	GGAAAG	aatacttaca
tctgctccca	TGGTGT	Exon 3	(187bp)	ATGCAG	gtccgagatg
ctgaatacag	ATCCTC	Exon 4	(73bp)	ATGCAG	gtgtcaggca
acttttcaag	ACCTAA	Exon 5	(34bp)	AGACAG	gtgagtcttt
ctcctccgta	GGCTGC	Exon 6	(101bp)	CTCCAG	ccccaggccc
cccactccag	CCCCAG	Exon 7	(109bp)	ACCCAG	acacctgtag
ccctgctcag	GTGCCG	*Exon 8	(22bp)	AGG**TGA**	...3'UTR

Fig.8B

36/52 Fig. 9(i)	37/52 Fig. 9(ii)
38/52 Fig. 9(iii)	39/52 Fig. 9(iv)

```
-163   gcacgagctcaggccgtcgctgcggcgctg
-103   gggggccgcggaggagccgccccctgcgcc
 -43   ggcggctctggctgacccccccccacaccg

  16   CGTCGCCTGCTGCTTGTTGCACTGCTGCAG
         R  R  L  L  L  V  A  L  L  Q

  76   TTTGATGGCCCCAGTCACCAGAAGAAAGTG
         F  D  G  P  S  H  Q  K  K  V

 136   ACATGCCAGCCCAGGGAGGTGGTGGTGCCT
         T  C  Q  P  R  E  V  V  V  P

 196   AAACAACTAGTGCCCAGCTGTGTGACTGTG
         K  Q  L  V  P  S  C  V  T  V

 256   GGCCTGGAATGTGTGCCCACTGGGCAACAC
         G  L  E  C  V  P  T  G  Q  H

 316   TACCCGAGCAGTCAGCTGGGGGAGATGTCC
         Y  P  S  S  Q  L  G  E  M  S

 376   CCTAAAAAAAAGGAGAGTGCTGTGAGGCCA
         P  K  K  K  E  S  A  V  R  P

 436   CAGCCCCGCTCTGTTCCGGGCTGGGACTCT
         Q  P  R  S  V  P  G  W  D  S
```

Fig.9(i)

```
cgttgcgctgcctgcgcccagggctcggga
ccgccccgggtccccgggtccgcgccatgg
ccgggctagggcccgATGAGCCCCCTGCTG
                M  S  P  L  L    -17

CTGGCTCGCACCCAGGCCCCTGTGTCCCAG
 L  A  R  T  Q  A  P  V  S  Q     4

GTGCCATGGATAGACGTTTATGCACGTGCC
 V  P  W  I  D  V  Y  A  R  A    24

CTGAGCATGGAACTCATGGGCAATGTGGTC
 L  S  M  E  L  M  G  N  V  V    44

CAGCGCTGTGGTGGCTGCTGCCCTGACGAT
 Q  R  C  G  G  C  C  P  D  D    64

CAAGTCCGAATGCAGATCCTCATGATCCAG
 Q  V  R  M  Q  I  L  M  I  Q    84

CTGGGAGAACACAGCCAATGTGAATGCAGA
 L  G  E  H  S  Q  C  E  C  R   104

GACAGGGTTGCCATACCCCACCACCGTCCC
 D  R  V  A  I  P  H  H  R  P   124

ACCCCGGGAGCACCCTCCCCAGCTGACATC
 T  P  G  A  P  S  P  A  D  I   144
```

Fig.9(ii)

```
496   ATCCATCCCACTCCAGCCCCAGGATCCTCT
        I  H  P  T  P  A  P  G  S  S
                       S  P  R  I  L

556   CTGACCCCCGGACCTGCCGTTGCCGCTGTA
        L  T  P  G  P  A  V  A  A  V
      P  D  P  R  T  C  R  C  R  C

616   GGGGCTTAGAGCTCAACCCAGACACCTGTA
        G  A  *
      R  G  L  E  L  N  P  D  T  C

676   ctttccagactccacgggcccggctgctttt
736   agcacaggcgtaacctcctcagtctgggag
796   gagctctctcgccatcttttatctcccaga
856   atgtctcacctcaggggccagggtactctc
916   ttctggctggctgtctcccctcactatgaa
976   gggttctgttatgataactgtgacacacac
1036  gacactaaaaaaaaaaaaaaaaaaaaaaa
```

Fig.9(iii)

```
GCCCGCCTTGCACCCAGCGCCGCCAACGCC
 A  R  L  A  P  S  A  A  N  A      164
C  P  P  C  T  Q  R  R  Q  R       130

GACGCCGCCGCTTCCTCCATTGCCAAGGGC
 D  A  A  A  S  S  I  A  K  G      184
R  R  R  R  F  L  H  C  Q  G       150

GGTGCCGGAAGCCGCGAAAGTGAcaagctg
                                   186
R  C  R  K  P  R  K  *             167

tatggccctgcttcacagggagaagagtgg
gtcactgccccaggacctggacctttttaga
gctgccatctaacaattgtcaaggaacctc
tcacttaaccaccctggtcaagtgagcatc
aaccccaaacttctaccaataacgggattt
acacactcacactctgataaaagagatgga
aaaaaaaaaaaa
```

Fig.9(iv)

40/52

41/52 Fig 10(i)	42/52 Fig 10(ii)

A

```
hVRF167   -21 MSPLLRRLLLAALLQLAPAQAP
              |||||||||||||||||||  |||
mVRF167   -21 MSPLLRRLLLVALLQLARTQAP

hVRF167    30 EVVVPLTVELMGTVAKQLVPSC
              ||||||  :||||  |  |||||||
mVRF167    30 EVVVPLSMELMGNVVKQLVPSC

hVRF167    80 ILMIRYPSSQLGEMSLEEHSQC
              ||||  ||||||||||||:|||||
mVRF167    80 ILMIQYPSSQLGEMSLGEHSQC

hVRF167   130 RPDPRTCRCRCRRRSFLRCQGR
              ||||||||||||||| ||:||||
mVRF167   130 RPDPRTCRCRCRRRRFLHCQGR
```

B

```
hVRF186   116 RAATPHHRPQPRSVPGWDSAPG
              | |||||||||||||||||| ||
mVRF186   116 RVAIPHHRPQPRSVPGWDSTPG

hVRF186   166 TPGPAAAAADAAASSVAKGGA*
              |||||  ||  ||||||:|||||
mVRF186   166 TPGPAVAAVDAAASSIAKGGA*
```

Fig.10(i)

```
VSQPDAPGHQRKVVSWIDVYTRATCQPR  29
|||  |:|:||:|||  |||||  |||||||
VSQFDGPSHQKKVVPWIDVYARATCQPR  29

VTVQRCGGCCPDDGLECVPTGQHQVRMQ  79
|||||||||||||||||||||||||||||
VTVQRCGGCCPDDGLECVPTGQHQVRMQ  79

ECRPKKKDSAVKPDSPRPLCPRCTQHHQ 129
|||||||:|||:|||||  |||  |||::|
ECRPKKKESAVRPDSPRILCPPCTQRRQ 129

GLELNPDTCRCRKLRR* 167
|||||||||||||||:
GLELNPDTCRCRKPRK* 167



APSPADITHPTPAPGPSAHAAPSTTSAL 165
|||||||  |||||||  ||:  |||    ||
APSPADIIHPTPAPGSSARLAPSAANAL 165

186

186
```

Fig.10(ii)

43/52

44/52

Fig 11(i)

45/52

Fig 11(ii)

```
mVRF167    -21 MSPLLRRL..LLVALLQL..
                |  ||  ::    |: ||  |
mVEGF188   -26 MNFLLSWVHWTLALLLYLHH

mVRF167     25 TCQPREVVVPLSMELMGNVV
                 | | | :| :  |  :::
mVEGF188    24 YCRPIETLVDIFQEYPDEIE

mVRF167     75 QVRMQILMIQYPSSQ.LGEM
                : |||: |     || :|||
mVEGF188    74 NITMQIMRIKPHQSQHIGEM

mVRF167    119 ..............ILCPPC
                             : | ||
mVEGF188   124 QKRKRKKSRFKSWSVHCEPC

mVRF167    152 GLELNPDTCRCRKPRK
                |||| |||| |||:
mVEGF188   173 QLELNERTCRCDKPRR
```

Fig.11(i)

```
AR.TQAPVSQFDGPSHQKKVVPWIDVYARA      24
|:  ||:     :|  : : |: ::|||  |
AKWSQAAPTT.EGEQKSHEVIKFMDVYQRS      23

KQLVPSCVTVQRCGGCCPDDGLECVPTGQH      74
  : |||| : ||:||| |::|||||||::
YIFKPSCVPLMRCAGCCNDEALECVPTSES      73

SLGEHSQCECRPKKKESAVRPDSPR.....      118
|: :|| |||||||          | |
SFLQHSRCECRPKKDRTKPEKKSVRGKGKG      123

TQRRQR...PDPRTCRCRCRRRRFLHCQGR      151
 :|| :    || ||:| |:      :| :|
SERRKHLFVQDPQTCKCSCKNTDS.RCKAR      172

                                    167

                                    188
```

Fig. 11(ii)

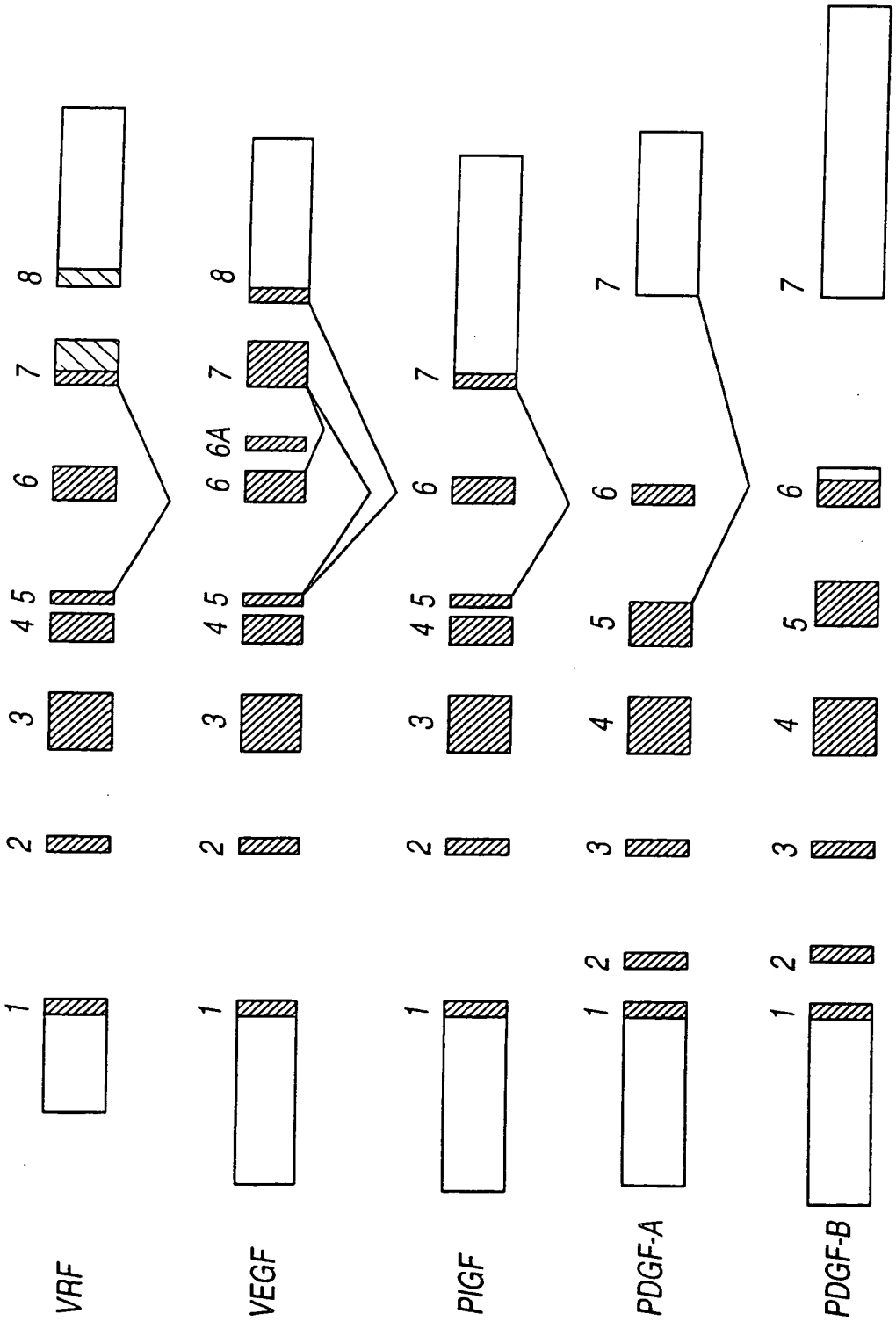


Fig.12

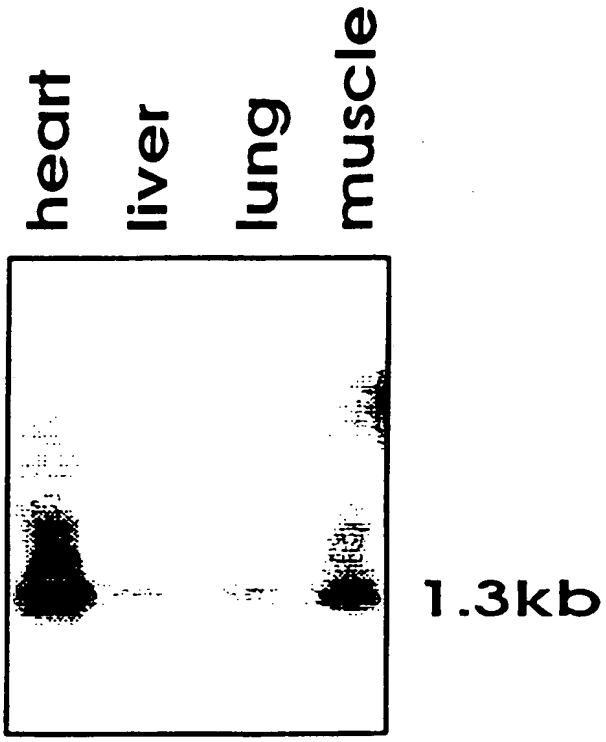


Fig.13

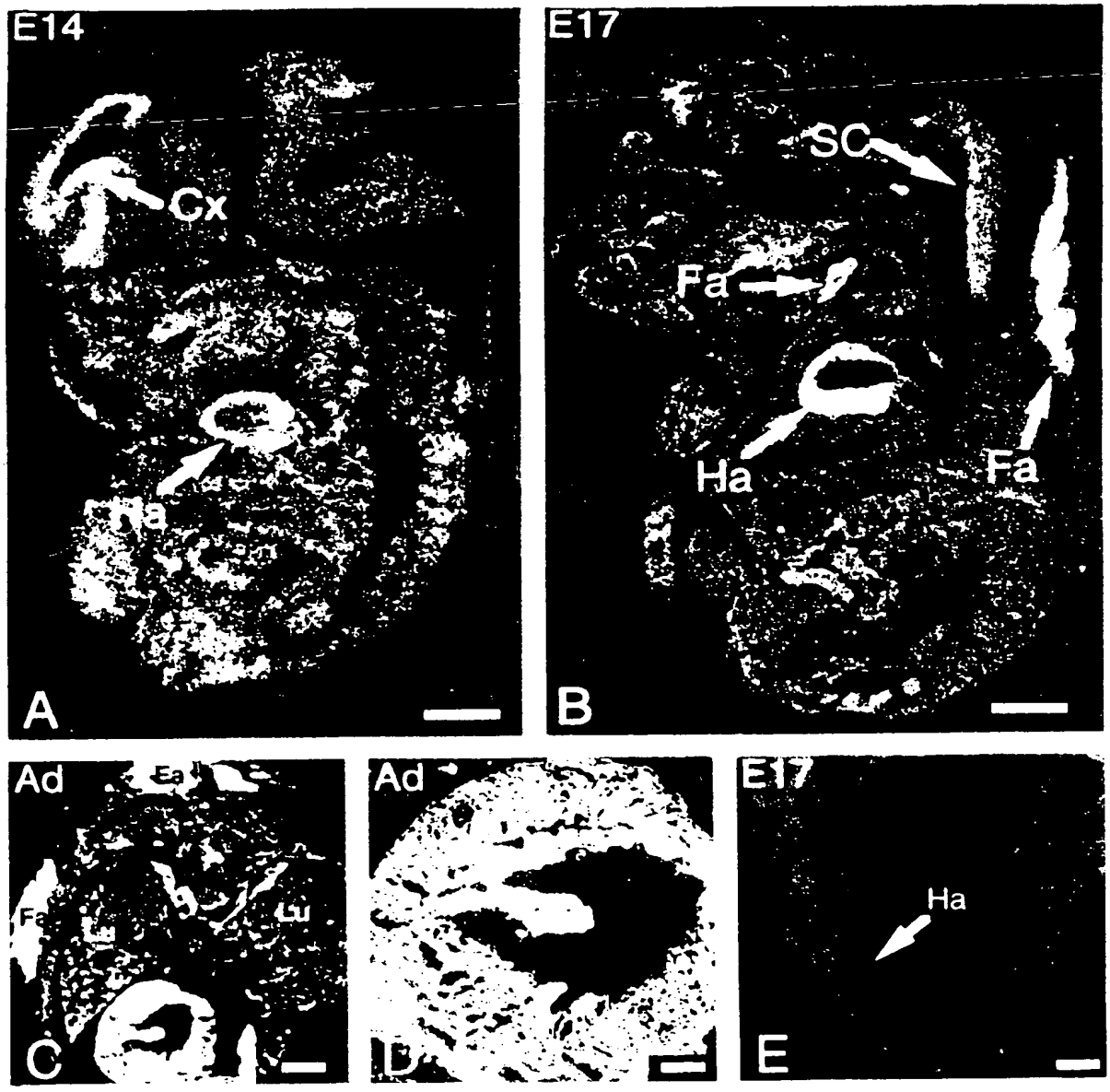


Fig.14

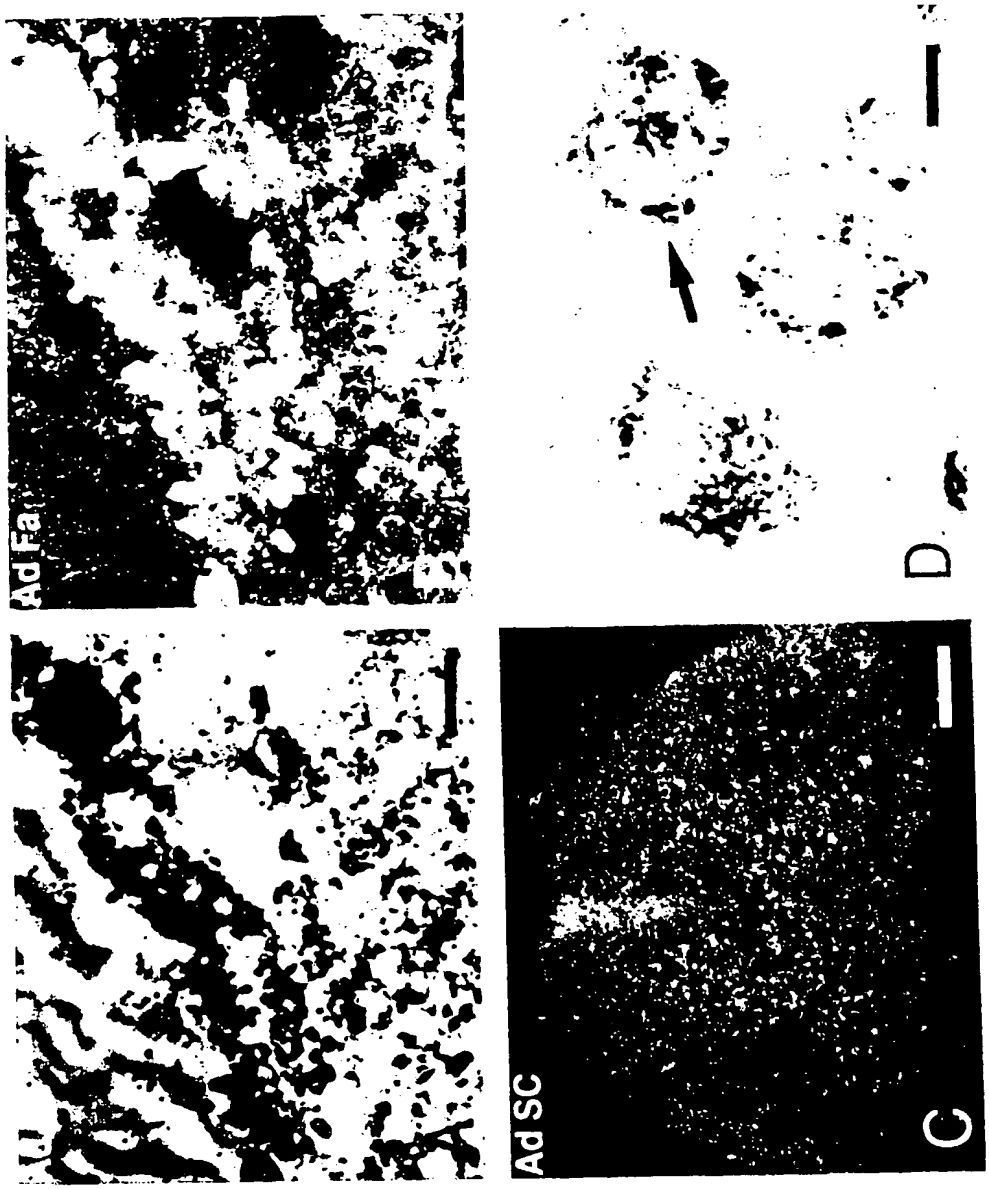


Fig. 15

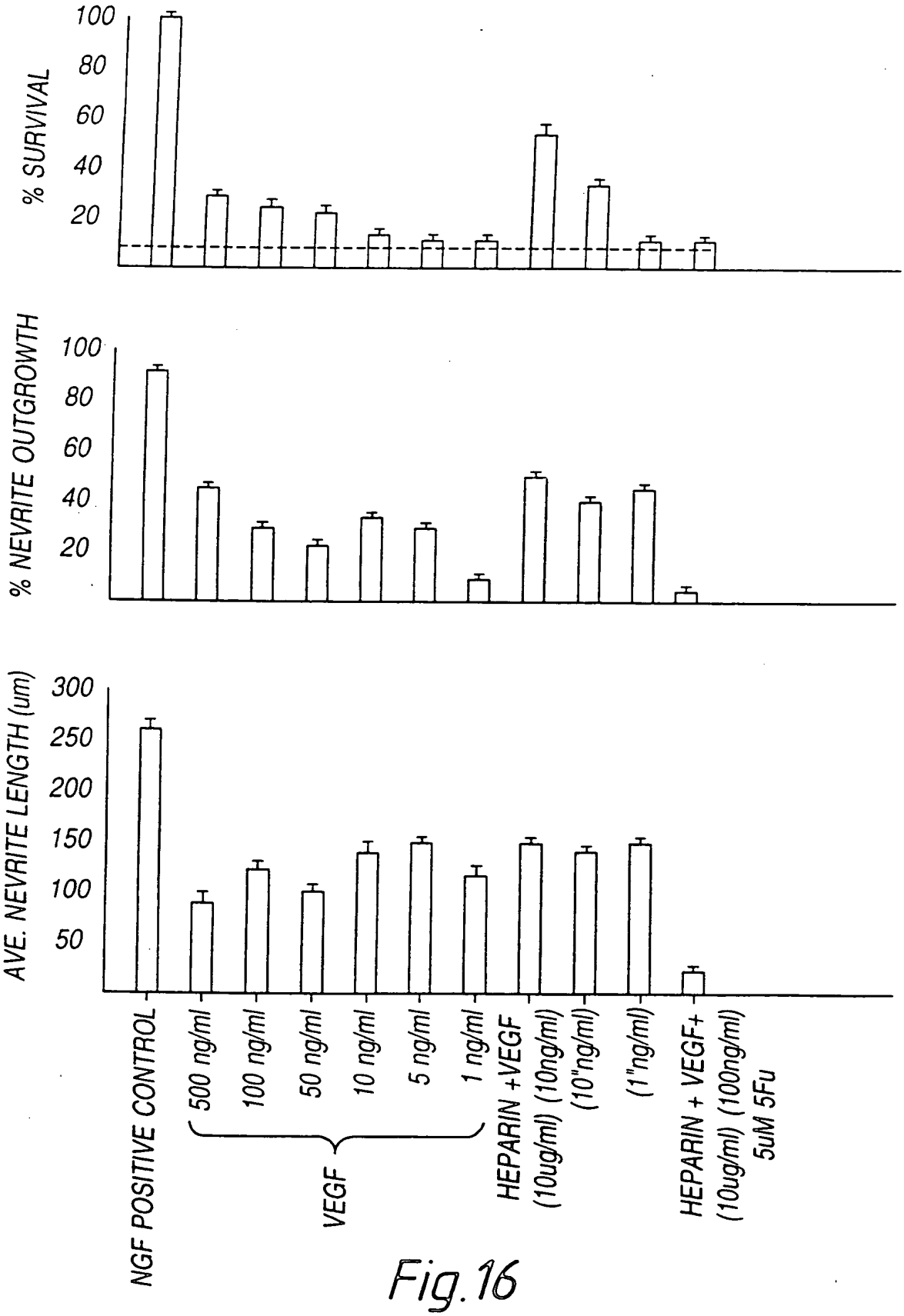


Fig. 16

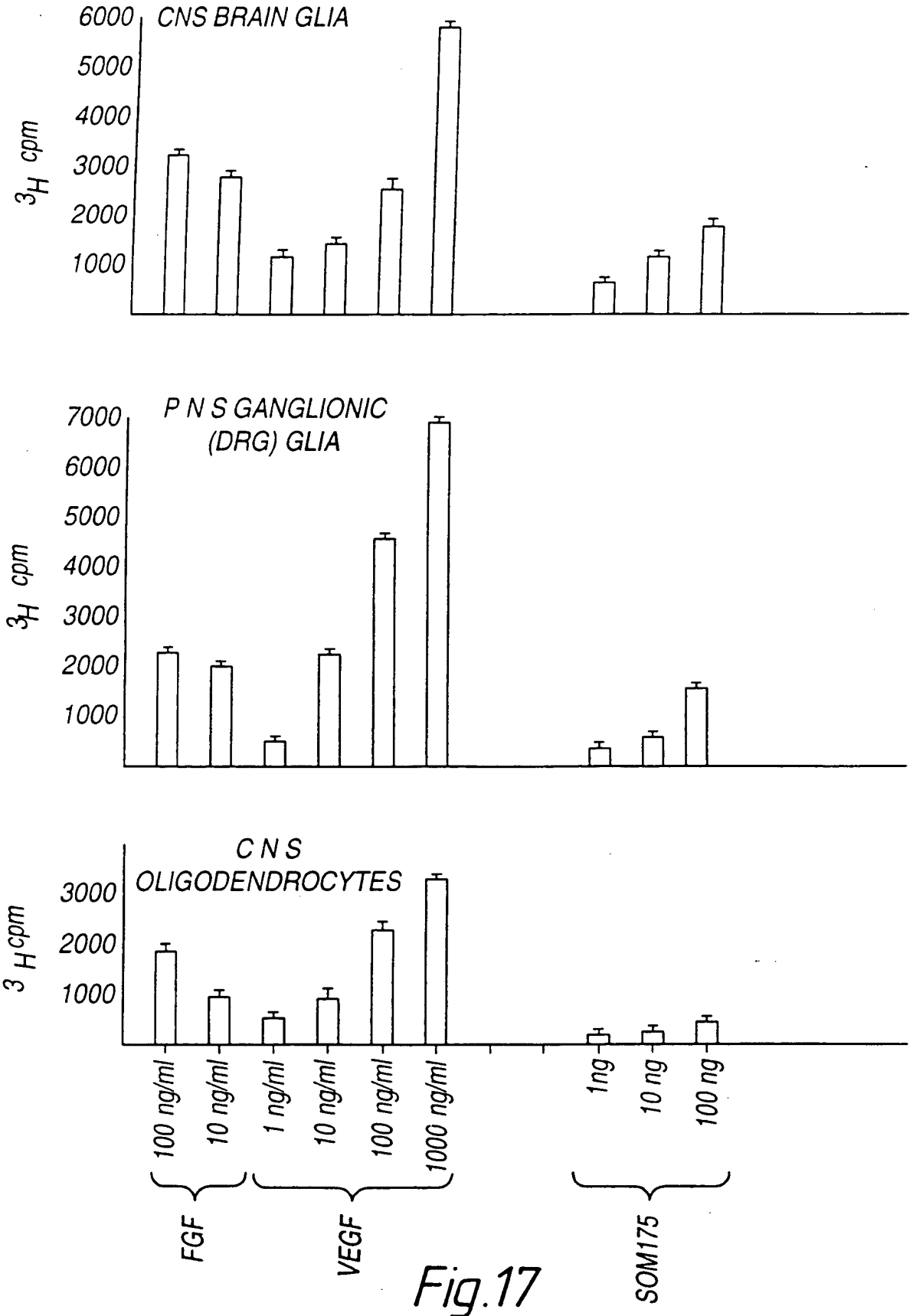


Fig.17

08/765588
PCT/AU96/00094

MOUSE ASTROGLIAL CELLS

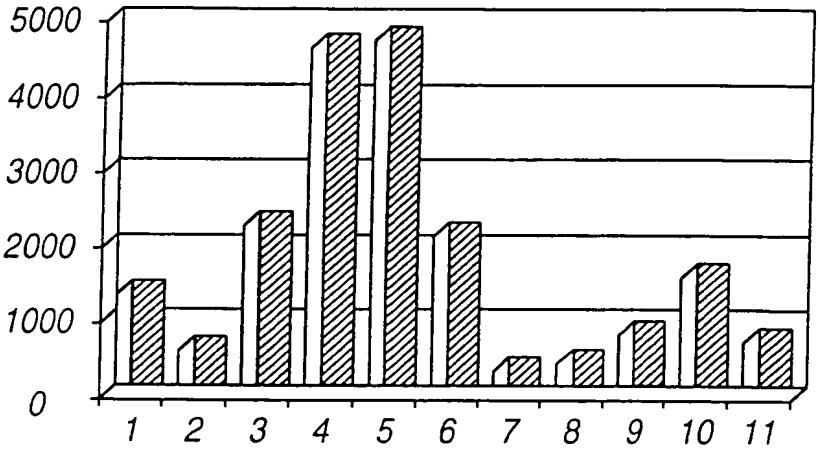


Fig.18

MOUSE OLIGODENDROGLIAL CELLS

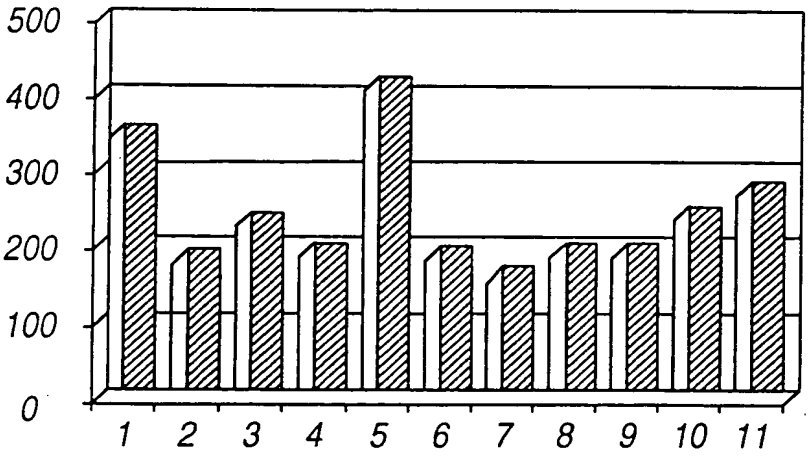


Fig.19

MOUSE FOREBRAIN NEURONS

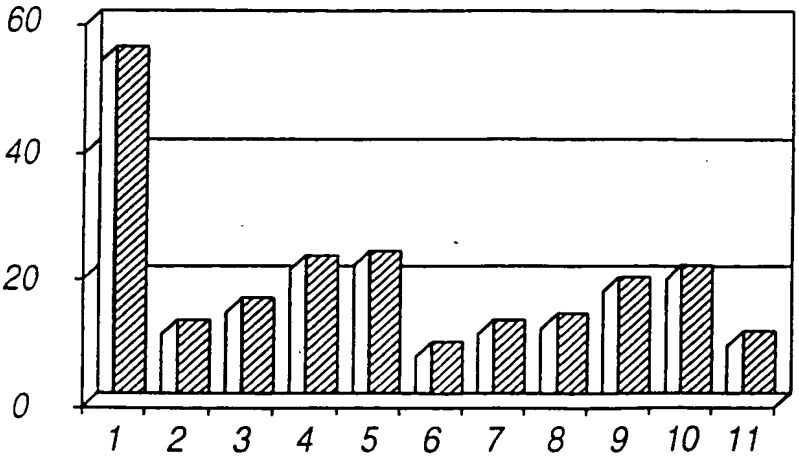


Fig.20